

SEQUENCE LISTING

<110> Galdes, Alphonse
Mahanthappa, Nagesh

<120> METHODS AND COMPOSITIONS FOR TREATING DISORDERS INVOLVING EXCITOTOXICITY

<130> BIV-069.02

<140> 09/325,602
<141> 1999-06-03

<150> 09/238,243
<151> 1999-01-27

<160> 32

<170> PatentIn Ver. 2.1

<210> 1

<211> 1277

<212> DNA

<213> Gallus sp.

<220>

<221> CDS

<222> (1), (1275)

<400> 1

```

atg gtc gaa atg ctg ctg ttg aca aga att ctc ttg gtg ggc ttc atc
Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
   1           5           10          15

```

tgc gct ctt tta gtc tcc tct ggg ctg act tgt gga cca ggc agg ggc 96
 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
 20 25 30

att gga aaa agg agg cac ccc aaa aag ctg acc ccg tta gcc tat aag 144
Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
35 40 45

cag ttt att ccc aat gtg gca gag aag acc cta ggg gcc agt gga aga 192
 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
 50 55 60

tat gaa ggg aag atc aca aga aac tcc gag aga ttt aaa gaa cta acc 240
 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
 65 70 75 80

cca aat tac aac cct gac att att ttt aag gat gaa gag aac acg gga 288
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
85 90 95

gct gac aga ctg atg act cag cgc tgc aag gac aag ctg aat gcc ctg 336
 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
 100 105 110

gct atc tcg gtg atg aac cag tgg ccc ggg gtg aag ctg cgg gtg acc Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr 115 120 125	384
gat ggc tgg gac gag gat ggc cat cac tcc gag gaa tcg ctg cac tac Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr 130 135 140	432
gag ggt cgc gcc gtg gac atc acc acg tcg gat cgg gac cgc agc aag Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys 145 150 155 160	480
tac gga atg ctg gcc cgc ctc gcc gtc gag gcc ggc ttc gac tgg gtc Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val 165 170 175	528
tac tac gag tcc aag gcg cac atc cac tgc tcc gtc aaa gca gaa aac Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn 180 185 190	576
tca gtg gca gcg aaa tca gga ggc tgc ttc cct ggc tca gcc aca gtg Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val 195 200 205	624
cac ctg gag cat gga ggc acc aag ctg gtg aag gac ctg agc cct ggg His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly 210 215 220	672
gac cgc gtg ctg gct gct gac gcg gac ggc cgg ctg ctc tac agt gac Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp 225 230 235 240	720
ttc ctc acc ttc ctc gac cgg atg gac agc tcc cga aag ctc ttc tac Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr 245 250 255	768
gtc atc gag acg cgg cag ccc cgg gcc cgg ctg cta ctg acg gcg gcc Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala 260 265 270	816
cac ctg ctc ttt gtg gcc ccc cag cac aac cag tcg gag gcc aca ggg His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly 275 280 285	864
tcc acc agt ggc cag gcg ctc ttc gcc agc aac gtg aag cct ggc caa Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln 290 295 300	912
cgt gtc tat gtg ctg ggc gag ggc ggg cag cag tcg ctg ctc ccg gcg tct Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser 305 310 315 320	960
gtc cac agc gtc tca ttg cgg gag gag gcg tcc gga gcc tac gcc cca Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro 325 330 335	1008

ctc acc gcc cag ggc acc atc ctc atc aac cggttggcc tcc tgc Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys 340 345 350	1056
tac gcc gtc atc gag gag cac agt tgg gcc cat tgg gcc ttc gca cca Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro 355 360 365	1104
ttc cgc ttg gct cag ggg ctg ctg gcc gcc ctc tgc cca gat ggg gcc Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala 370 375 380	1152
atc cct act gcc gcc acc acc act ggc atc cat tgg tac tca cgg Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg 385 390 395 400	1200
ctc ctc tac cgc atc ggc agc tgg gtg ctg gat ggt gac gcg ctg cat Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His 405 410 415	1248
ccg ctg ggc atg gtg gca ccg gcc agc tg Pro Leu Gly Met Val Ala Pro Ala Ser 420 425	1277
<210> 2	
<211> 1190	
<212> DNA	
<213> Murine sp.	
<220>	
<221> CDS	
<222> (1)...(1188)	
 <400> 2	
atg gct ctg ccc agt ctg ttg ccc ctg tgc tgc ttg gca ctc ttg Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu 1 5 10 15	48
gca cta tct gcc cag agc tgc ggg ccg ggc cga gga ccg gtt ggc cgg Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg 20 25 30	96
cggtatgtcgcaaaactgttctctatcacaaagcaggaccctgtggccatcataaagcaggat Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe 35 40 45	144
gtgtcccatgtcccaggccgttgcggccatgtggccatgtggccatgtggccatgtggccatgtggcc Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu 50 55 60	192
ggagggtacaacaaggggtcggagccatgtggccatgtggccatgtggccatgtggccatgtggcc Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn 65 70 75 80	240
tac aac ccc gac ata atc ttc aag gat gag gag aac agc ggc gca gac Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp 85 90 95	288

cgc ctg atg aca gag cgt tgc aaa gag cg ^g gtg aac gct cta gcc atc Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile 100	105	110	336	
g ^c g gtg atg aac atg tgg ccc gga gta cgc cta cgt gtg act gaa ggc Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly 115	120	125	384	
tgg gac gag gac ggc cac cac gca cag gat tca ctc cac tac gaa ggc Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly 130	135	140	432	
cgt gcc ttg gac atc acc acg tct gac cgt gac cgt aat aag tat ggt Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly 145	150	155	160	480
ttg ttg gcg cgc cta gct gtg gaa gcc gga ttc gac tgg gtc tac tac Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr 165	170	175	528	
gag tcc cgc aac cac atc cac gta tcg gtc aaa gct gat aac t ^c a ctg Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu 180	185	190	576	
g ^c g gtc cga gcc gga ggc tgc ttt cc ^g gga aat gcc acg gtg cgc ttg Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu 195	200	205	624	
cgg agc ggc gaa cgg aag ggg ctg agg gaa cta cat cgt ggt gac tgg Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp 210	215	220	672	
gta ctg gcc gct gat gca g ^c g ggc cga gtg gta ccc acg cca gtg ctg Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu 225	230	235	240	720
ctc ttc ctg gac cgg gat ctg cag cgc cgc gcc tcg ttc gtg gct gtg Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val 245	250	255	768	
gag acc gag cgg cct cc ^g cgc aaa ctg ttg ctc aca ccc tgg cat ctg Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu 260	265	270	816	
gtg ttc gct gct cgc ggg cca g ^c g cct gct cca ggt gac ttt gca cc ^g Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro 275	280	285	864	
gtg ttc g ^c g cgc cgc tta cgt gct ggc gac tcg gtg ctg gct ccc ggc Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly 290	295	300	912	
ggg gac g ^c g ctc cag cc ^g g ^c g cgc gta gcc cgc gtg g ^c g cgc gag gaa Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu 305	310	315	320	960

gcc gtg ggc gtg ttc gca ccg ctc act	gcg cac ggg acg ctg ctg gtc	1008
Ala Val Gly Val Phe Ala Pro Leu Thr	Ala His Gly Thr Leu Leu Val	
325	330	335
aac gac gtc ctc gcc tcc tgc tac	gct cta gag agt cac cag tgg	1056
Asn Asp Val Leu Ala Ser Cys Tyr	Ala Val Leu Glu Ser His Gln Trp	
340	345	350
gcc cac cgc gcc ttc gcc cct ttg	cgg ctg ctg cac ggc ctc ggg gct	1104
Ala His Arg Ala Phe Ala Pro Leu Arg	Leu His Ala Leu Gly Ala	
355	360	365
ctg ctc cct ggg ggt gca gtc cag	ccg act ggc atg cat tgg tac tct	1152
Leu Leu Pro Gly Gly Ala Val Gln Pro	Thr Gly Met His Trp Tyr Ser	
370	375	380
cgc ctc ctt tac cgc ttg gcc gag	gag tta atg ggc tg	1190
Arg Leu Leu Tyr Arg Leu Ala Glu	Glu Leu Met Gly	
385	390	395
<210> 3		
<211> 1281		
<212>, DNA		
<213> Murine sp.		
<220>		
<221> CDS		
<222> (1)..(1233)		
<400> 3		
atg tct ccc gcc tgg ctc cgg ccc cga	ctg cgg ttc tgt ctg ttc ctg	48
Met Ser Pro Ala Trp Leu Arg Pro Arg	Leu Arg Phe Cys Leu Phe Leu	
1	5	10
ctg ctg ctg ctt ctg gtg ccg gcg	cg cg gg tc ggg ccg gg cc gg	96
Leu Leu Leu Leu Val Pro Ala Ala Arg	Gly Cys Gly Pro Gly Arg	
20	25	30
gtg gtg ggc agc cgc cgg agg	ccg cct ctc gtg cct ctt gcc	144
Val Val Gly Ser Arg Arg Pro Pro Arg	Lys Leu Val Pro Leu Ala	
35	40	45
tac aag cag ttc agc ccc aac	gtg ccg gag aag acc ctg ggc gcc agc	192
Tyr Lys Gln Phe Ser Pro Asn Val	Pro Glu Lys Thr Leu Gly Ala Ser	
50	55	60
ggg cgc tac gaa ggc aag atc	gct gag cgc ttc aaa gag	240
Gly Arg Tyr Glu Gly Lys Ile Ala Arg	Ser Ser Glu Arg Phe Lys Glu	
65	70	75
ctc acc ccc aac tac aat ccc gac	atc atc ttc aag gac gag gag aac	288
Leu Thr Pro Asn Tyr Asn Pro Asp	Ile Ile Phe Lys Asp Glu Glu Asn	
85	90	95
acg ggt gcc gac cgc ctc atg acc	cag cgc tgc aag gac cgt ctg aac	336
Thr Gly Ala Asp Arg Leu Met Thr	Gln Arg Cys Lys Asp Arg Leu Asn	
100	105	110

tca ctg gcc atc tct gtc atg aac cag tgg cct ggt gtg aaa ctg cg		384	
Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg			
115	120	125	
gtg acc gaa ggc cg gat gaa gat ggc cat cac tca gag gag tct tta		432	
Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu			
130	135	140	
cac tat gag ggc cgc gcg gtg gat atc acc acc tca gac cgt gac cga		480	
His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg			
145	150	155	160
aat aag tat gga ctg ctg gcg tta gca gtg gag gcc ggc ttc gac		528	
Asn Lys Tyr Glu Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp			
165	170	175	
tgg gtg tat tac gag tcc aag gcc cac gtg cat tgc tct gtc aag tct		576	
Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser			
180	185	190	
gag cat tcg gcc gct gcc aag aca ggt ggc tgc ttt cct gcc gga gcc		624	
Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala			
195	200	205	
cag gtg cgc cta gag aac ggg gag cgt gtg gcc ctg tca gct gta aag		672	
Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys			
210	215	220	
cca gga gac cgg gtg ctg gcc atg ggg gag gat ggg acc ccc acc ttc		720	
Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe			
225	230	235	240
agt gat gtg ctt att ttc ctg gac cgc gag cca aac cgg ctg aga gct		768	
Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala			
245	250	255	
ttc cag gtc atc gag act cag gat cct ccg cgt cgg ctg gcg ctc acg		816	
Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr			
260	265	270	
cct gcc cac ctg ctc ttc att gcg gac aat cat aca gaa cca gca gcc		864	
Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala			
275	280	285	
cac ttc cgg gcc aca ttt gcc agc cat gtg caa cca ggc caa tat gtg		912	
His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val			
290	295	300	
ctg gta tca ggg gta cca ggc ctc cag cct gct cgg gtg gca gct gtc		960	
Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val			
305	310	315	320
tcc acc cac gtg gcc ctt ggg tcc tat gct cct ctc aca agg cat ggg		1008	
Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly			
325	330	335	

aca ctt gtg gtg gag gat gtg gtg gcc tcc tgc ttt gca gct gtc gtc	1056
Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala	
340 345 350	
gac cac cat ctg gct cag ttg gcc ttc tgg ccc ctg cga ctg ttt ccc	1104
Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro	
355 360 365	
agt ttg gca tgg ggc agc tgg acc cca agt gag ggt gtt cac tcc tac	1152
Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr	
370 375 380	
cct cag atg ctc tac cgc ctg ggg cgt ctc ttg cta gaa gag agc acc	1200
Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Ser Thr	
385 390 395 400	
ttc cat cca ctg ggc atg tct ggg gca gga agc tgaaggact ctaaccactg	1253
Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser	
405 410	
ccctcctgga actgctgtgc gtggatcc	1281

<210> 4
<211> 1313
<212> DNA
<213> Murine sp.

<220>
<221> CDS
<222> (1)...(1311)

<400> 4				
atg ctg ctg ctg ctg gcc aga tgt ttt ctg gtg atc ctt gct tcc tcg	48			
Met Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser				
1 5 10 15				
ctg ctg gtg tgc ccc ggg ctg gcc tgt ggg ccc ggc agg ggg ttt gga	96			
Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly				
20 25 30				
aag agg cgg cac ccc aaa aag ctg acc cct tta gcc tac aag cag ttt	144			
Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe				
35 40 45				
att ccc aac gta gcc gag aag acc cta ggg gcc agc ggc aga tat gaa	192			
Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu				
50 55 60				
ggg aag atc aca aga aac tcc gaa cga ttt aag gaa ctc acc ccc aat	240			
Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn				
65 70 75 80				
tac aac ccc gac atc ata ttt aag gat gag gaa aac acg gga gca gac	288			
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp				
85 90 95				

cggtgcatcactcagaggttcggaaaacaaatgttgcgttgcgtccatc Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile	336
100 105 110	
tctgtatgAACcAGTGGCCTGGAGGCTGCGAGGTGGACCGAGGG Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	384
115 120 125	
tggatgagGACGGCCATCATTCAGAGGAGTCTCTACATGAGGGT Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly	432
130 135 140	
cga gca gtg gac atc acc acg tcc gac cgg gac cgc agc aag tac ggc Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly	480
145 150 155 160	
atgctgcgtcgcctgtgtggaaGCAggTTGACtgggtc tac tat Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	528
165 170 175	
gaa tcc aaa gct cac atc cac tgt tct gtg aaa gca gag aac tcc gtg Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val	576
180 185 190	
gcg gcc aaa tcc ggc ggc tgt ttc ccg gga tcc gcc acc gtg cac ctg Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu	624
195 200 205	
gag cag ggc acc aag ctg gtg aag gac tta cgt ccc gga gac cgc Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg	672
210 215 220	
gtgctgcgtgacgac cagggccgtctgtacagc gac ttc ctc Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu	720
225 230 235 240	
acc ttc ctg gac cgc gac gaa ggc gcc aag aag gtc ttc tac gtg atc Thr Phe Leu Asp Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile	768
245 250 255	
gag acg ctg gag ccg cgc gag cgc ctg ctc acc gcc gcg cac ctg Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu	816
260 265 270	
ctcttcgtgcgcacaacgactcggggcccacggccccaagc Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser	864
275 280 285	
gcgcgcgttgcgcgtcccccggcagcgcgtgtacgttgt Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val	912
290 295 300	
gctgaa cgc ggc ggg gac cgc cgg ctg ctc acc gcc gcg gtg cac agc Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser	960
305 310 315 320	

gtg acg ctg cga gag gag ggc ggc tac gcg ccg ctc acg gcg Val Thr Leu Arg Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala	325	330	335	1008
cac ggc acc att ctc atc aac cgg gtg ctc gcc tgc tac gct gtc His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val	340	345	350	1056
atc gag gag cac agc tgg gca cac cgg gcc ttc gcg cct ttc cgc ctg Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu	355	360	365	1104
gcg cac gcg ctg ctg gcc gcg ctg gca ccc gcc cgc acg gac ggc ggg Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly	370	375	380	1152
ggc ggg ggc agc atc cct gca gcg caa tct gca acg gaa gcg agg ggc Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly	385	390	395	400
gcg gag ccg act gcg ggc atc cac tgg tac tgc cag ctg ctc tac cac Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His	405	410	415	1248
att ggc acc tgg ctg ttg gac agc gag acc atg cat ccc ttg gga atg Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met	420	425	430	1296
gcg gtc aag tcc agc tg Ala Val Lys Ser Ser	435			1313
<210> 5				
<211> 1256				
<212> DNA				
<213> Brachydanio rerio				
<220>				
<221> CDS				
<222> (1)..(1254)				
<400> 5				
atg cgg ctt ttg acg aga gtg ctg ctg gtg tct ctt ctc act ctg tcc Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser	1	5	10	15
ttg gtg gtg tcc gga ctg gcc tgc ggt cct ggc aga ggc tac ggc aga Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg	20	25	30	48
aga aga cat ccg aag aag ctg aca cct ctc gcc tac aag cag ttc ata Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile	35	40	45	96
cct aat gtc gcg gag aag acc tta ggg gcc agc ggc aga tac gag ggc Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly	50	55	60	144
				192

aag ata acg cgc aat tcg gag aga ttt aaa gaa ctt act cca aat tac Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr 65 70 75 80	240
aat ccc gac att atc ttt aag gat gag gag aac acg gga gcg gac agg Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg 85 90 95	288
ctc atg aca cag aga tgc aaa gac aag ctg aac tcg ctg gcc atc tct Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser 100 105 110	336
gta atg aac cac tgg cca ggg gtt aag ctg cgt gtg aca gag ggc tgg Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp 115 120 125	384
gat gag gac ggt cac cat ttt gaa gaa tca ctc cac tac gag gga aga Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg 130 135 140	432
gct gtt gat att acc acc tct gac cga gac aag agc aaa tac ggg aca Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr 145 150 155 160	480
ctg tct cgc cta gct gtg gag gct gga ttt gac tgg gtc tat tac gag Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu 165 170 175	528
tcc aaa gcc cac att cat tgc tct gtc aaa gca gaa aat tcg gtt gct Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala 180 185 190	576
gcg aaa tct ggg ggc tgt ttc cca ggt tcg gct ctg gtc tcg ctc cag Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln 195 200 205	624
gac gga gga cag aag gcc gtg aag gac ctg aac ccc gga gac aag gtg Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val 210 215 220	672
ctg gcg gca gac agc gcg gga aac ctg gtg ttc agc gac ttc atc atg Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met 225 230 235 240	720
ttc aca gac cga gac tcc acg acg cga cgt gtg ttt tac gtc ata gaa Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu 245 250 255	768
acg caa gaa ccc gtt gaa aag atc acc ctc acc gcc gct cac ctc ctt Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu 260 265 270	816
ttt gtc ctc gac aac tca acg gaa gat ctc cac acc atg acc gcc gcg Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala 275 280 285	864

tat gcc agc agt gtc aga gca aag gtg atg gtt gat gat Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp	912
290 295 300	
 agc ggt cag ctt aaa tct gtc atc gtg cag cggtt gat tac acg gag gag Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu	960
305 310 315 320	
 cag cgg ggc tcg ttc gca cca gtg act gca cat ggg acc att gtg gtc Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val	1008
325 330 335	
 gac aga ata ctg gcg tcc tgt tac gcc gta ata gag gac cag ggg ctt Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu	1056
340 345 350	
 gcg cat ttg gcc ttc gcg ccc gcc agg ctc tat tat tac gtg tca tca Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Val Ser Ser	1104
355 360 365	
 ttc ctg tcc ccc aaa act cca gca gtc ggt cca atg cga ctt tac aac Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn	1152
370 375 380	
 agg agg ggg tcc act ggt act cca ggc tcc tgt cat caa atg gga acg Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr	1200
385 390 395 400	
 tgg ctt ttg gac agc aac atg ctt cat cct ttg ggg atg tca gta aac Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn	1248
405 410 415	
 tca agc tg Ser Ser	1256
 <210> 6	
<211> 1425	
<212> DNA	
<213> Homo sapien	
 <220>	
<221> CDS	
<222> (1)..(1425)	
 <220>	
<221> MOD_RES	
<222> (1397)..(1389)	
<223> a, t, c, g, other or unknown	
 <400> 6	
atg ctg ctg ctg gcg aga tgt ctg ctg cta gtc ctc gtc tcc tcg ctg Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu	48
1 5 10 15	
 ctg gta tgc tcg gga ctg gcg tgc gga ccg ggc agg ggg ttc ggg aag Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys	96
20 25 30	

agg agg cac ccc aaa aag ctg acc cct tta gcc tac aag cag ttt atc Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile	35	40	45	144
ccc aat gtg gcc gag aag acc cta ggc gcc agc gga agg tat gaa ggg Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly	50	55	60	192
aag atc tcc aga aac tcc gag cga ttt aag gaa ctc acc ccc aat tac Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr	65	70	75	240
aac ccc gac atc ata ttt aag gat gaa gaa aac acc gga gcg gac agg Asn Pro Asp Ile Ile Phe Lys Asp Glu Asn Thr Gly Ala Asp Arg	85	90	95	288
ctg atg act cag agg tgt aag gac aag ttg aac gct ttg gcc atc tcg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser	100	105	110	336
gtg atg aac cag tgg cca gga gtg aaa ctg cgg gtg acc gag ggc tgg Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp	115	120	125	384
gac gaa gat ggc cac cac tca gag gag tct ctg cac tac gag ggc cgc Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg	130	135	140	432
gca gtg gac atc acc acg tct gac cgc gac cgc agc aag tac ggc atg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Ser Lys Tyr Gly Met	145	150	155	480
ctg gcc cgc ctg gcg gtg gag gcc ggc ttc gac tgg gtg tac tac gag Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu	165	170	175	528
tcc aag gca cat atc cac tgc tcg gtg aaa gca gag aac tcg gtg gcg Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala	180	185	190	576
gcc aaa tcg gga ggc tgc ttc ccg ggc tcg gcc acg gtg cac ctg gag Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu	195	200	205	624
cag ggc ggc acc aag ctg gtg aag gac ctg agc ccc ggg gac cgc gtg Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val	210	215	220	672
ctg gcg gac gac cag ggc cgg ctg ctc tac agc gac ttc ctc act Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr	225	230	235	720
ttc ctg gac cgc gac gac ggc aag aag gtc ttc tac gtg atc gag Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu	245	250	255	768

acg	cgg	gag	ccg	cgc	gag	cgc	ctg	ctg	acc	gcc	gcg	cac	ctg	ctc		816	
Thr	Arg	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	Leu		
							260		265					270			
ttt	gtg	gcf	ccg	cac	aac	gac	tcg	gcc	acc	ggg	gag	ccc	gag	gcf	tcc	864	
Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Ala	Thr	Gly	Glu	Pro	Glu	Ala	Ser		
							275		280					285			
tcg	ggc	tcg	ggg	ccg	cct	tcc	ggg	ggc	gca	ctg	ggg	cct	cgf	gcf	ctg	912	
Ser	Gly	Ser	Gly	Pro	Pro	Ser	Gly	Gly	Ala	Leu	Gly	Pro	Arg	Ala	Leu		
							290		295					300			
ttc	gcc	agc	cgc	gtg	cgc	ccg	ggc	cag	cgc	gtg	tac	gtg	gtg	gcc	gag	960	
Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	Ala	Glu		
							305		310					315		320	
cgt	gac	ggg	gac	cgc	ccg	ctc	ctg	ccc	gcc	gct	gtg	cac	agc	gtg	acc	1008	
Arg	Asp	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser	Val	Thr		
							325		330					335			
cta	agc	gag	gag	gcc	gcf	ggc	gcc	tac	gcf	ccg	ctc	acg	gcc	cag	ggc	1056	
Leu	Ser	Glu	Glu	Ala	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala	Gln	Gly		
							340		345					350			
acc	att	ctc	atc	aac	cgf	gtg	ctg	gcc	tcg	tgc	tac	gcf	gtc	atc	gag	1104	
Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu		
							355		360					365			
gag	cac	agc	tgg	gcf	cac	ccg	ggc	ttc	gcf	ccc	ttc	ccg	ctg	gcf	cac	1152	
Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu	Ala	His		
							370		375					380			
gcf	ctc	ctg	gct	gca	ctg	gcf	ccc	gcf	ccg	acg	gac	ccg	ggc	ggg	gac	1200	
Ala	Leu	Leu	Ala	Ala	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Arg	Gly	Gly	Asp		
							385		390					395		400	
agc	ggc	ggg	gac	cgc	ggg	ggc	ggc	ggc	ggc	aga	gta	gcc	cta	acc		1248	
Ser	Gly	Gly	Asp	Arg	Gly	Gly	Gly	Gly	Gly	Gly	Arg	Val	Ala	Leu	Thr		
							405		410					415			
gct	cca	ggf	gct	gcc	gac	gct	ccg	ggf	gcf	ggg	gcc	acc	gcf	ggc	atc	1296	
Ala	Pro	Gly	Ala	Ala	Asp	Ala	Pro	Gly	Ala	Gly	Ala	Thr	Ala	Gly	Ile		
							420		425					430			
cac	tgg	tac	tcg	cag	ctg	ctc	tac	caa	ata	ggc	acc	tgg	ctc	ctg	gac	1344	
His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	Gln	Ile	Gly	Thr	Trp	Leu	Leu	Asp		
							435		440					445			
agc	gag	gcc	ctg	cac	ccg	ctg	ggc	atg	gcf	gtc	aag	tcc	agc	nnn	agc	1392	
Ser	Glu	Ala	Leu	His	Pro	Leu	Gly	Met	Ala	Val	Lys	Ser	Ser	Xaa	Ser		
							450		455					460			
cgf	ggg	gcc	ggg	gga	ggg	gcf	ccg	gag	ggg	gcc						1425	
Arg	Gly	Ala	Gly	Gly	Gly	Ala	Arg	Glu	Gly	Ala							
							465		470					475			

<210> 7
<211> 1622

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (51)..(1283)

<400> 7

catcagccca ccaggagacc tcgccccggc ctccccgggg ctcccccggcc atg tct	56
Met Ser	
1	

ccc gcc cgg ctc cg ccc cga ctg cac ttc tgc ctg gtc ctg ttg ctg	104		
Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu Leu Leu			
5	10	15	

ctg ctg gtg gtg ccc gcg gca tgg ggc tgc ggg ccg ggt cgg gtg gtg	152		
Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg Val Val			
20	25	30	

ggc agc cgc cgg cga ccg cca cgc aaa ctc gtg ccg ctc gcc tac aag	200		
Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala Tyr Lys			
35	40	45	50

cag ttc agc ccc aat gtg ccc gag aag acc ctg ggc gcc agc gga cgc	248		
Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser Gly Arg			
55	60	65	

tat gaa ggc aag atc gct cgc agc tcc gag cgc ttc aag gag ctc acc	296		
Tyr Glu Gly Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu Leu Thr			
70	75	80	

ccc aat tac aat cca gac atc atc ttc aag gac gag gag aac aca ggc	344		
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly			
85	90	95	

gcc gac cgc ctc atg acc cag cgc tgc aag gac cgc ctg aac tcg ctg	392		
Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn Ser Leu			
100	105	110	

gct atc tcg gtg atg aac cag tgg ccc ggt gtg aag ctg cgg gtg acc	440		
Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr			
115	120	125	130

gag ggc tgg gac gag gac ggc cac cac tca gag gag tcc ctg cat tat	488		
Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr			
135	140	145	

gag ggc cgc gcg gtg gac atc acc aca tca gac cgc gac cgc aat aag	536		
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys			
150	155	160	

tat gga ctg ctg gcg cgc ttg gca gtg gag gcc ggc ttt gac tgg gtg	584		
Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val			
165	170	175	

tat tac gag tca aag gcc cac gtg cat tgc tcc gtc aag tcc gag cac Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser Glu His 180 185 190	632
tcg gcc gca gcc aag acg ggc ggc tgc ttc cct gcc gga gcc cag gta Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala Gln Val 195 200 205 210	680
cgc ctg gag agt ggg gcg cgt gtg gcc ttg tca gcc gtg agg ccg gga Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg Pro Gly 215 220 225	728
gac cgt gtg ctg gcc atg ggg gag gat ggg agc ccc acc ttc agc gat Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe Ser Asp 230 235 240	776
gtg ctc att ttc ctg gac cgc gag ccc cac agg ctg aga gcc ttc cag Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala Phe Gln 245 250 255	824
gtc atc gag act cag gac ccc cca cgc cgc ctg gca ctc aca ccc gct Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr Pro Ala 260 265 270	872
cac ctg ctc ttt acg gct gac aat cac acg gag ccg gca gcc cgc ttc His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala Arg Phe 275 280 285 290	920
cgg gcc aca ttt gcc agc cac gtg cag cct ggc cag tac gtg ctg gtg Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val Leu Val 295 300 305	968
gct ggg gtg cca ggc ctg cag cct gcc cgc gtg gca gct gtc tct aca Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val Ser Thr 310 315 320	1016
cac gtg gcc ctc ggg gcc tac gcc ccg ctc aca aag cat ggg aca ctg His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly Thr Leu 325 330 335	1064
gtg gtg gag gat gtg gtg gca tcc tgc ttc gcg gcc gtg gct gac cac Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala Asp His 340 345 350	1112
cac ctg gct cag ttg gcc ttc tgg ccc ctg aga ctc ttt cac agc ttg His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His Ser Leu 355 360 365 370	1160
gca tgg ggc agc tgg acc ccg ggg gag ggt gtg cat tgg tac ccc cag Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr Pro Gln 375 380 385	1208
ctg ctc tac cgc ctg ggg cgt ctc ctg cta gaa gag ggc agc ttc cac Leu Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Gly Ser Phe His 390 395 400	1256

tgg gac gag gac ggc cac cac gct cag gat tca ctc cac tac gaa ggc Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	432
130 135 140	
cgt gct ttg gac atc act acg tct gac cgc gac cgc aac aag tat ggg Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly	480
145 150 155 160	
ttg ctg gcg cgc ctc gca gtg gaa gcc ggc ttc gac tgg gtc tac tac Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	528
165 170 175	
gag tcc cgc aac cac gtc cac gtg tcg gtc aaa gct gat aac tca ctg Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu	576
180 185 190	
gcg gtc cgg gcg ggc ggc tgc ttt ccg gga aat gca act gtg cgc ctg Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu	624
195 200 205	
tgg agc ggc gag cgg aaa ggg ctg cgg gaa ctg cac cgc gga gae tgg Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp	672
210 215 220	
gtt ttg gcg gcc gat gcg tca ggc cgg gtg ccc acg ccg gtg ctg Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu	720
225 230 235 240	
ctc ttc ctg gac cgg gac ttg cag cgc cgg gct tca ttt gtg gct gtg Leu Phe Leu Asp Arg Asp Leu Gln Arg Ala Ser Phe Val Ala Val	768
245 250 255	
gag acc gag tgg cct cca cgc aaa ctg ttg ctc acg ccc tgg cac ctg Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu	816
260 265 270	
gtg ttt gcc gct cga ggg ccg gcg ccc gca ggc gac ttt gca ccg Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro	864
275 280 285	
gtg ttc gcg cgc cgg cta cgc gct ggg gac tcg gtg ctg gcg ccc ggc Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly	912
290 295 300	
ggg gat gcg ctt cgg cca gcg cgc gtg gcc cgt gtg gcg cgg gag gaa Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu	960
305 310 315 320	
gcc gtg ggc gtg ttc gcg ccg ctc acc gcg cac ggg acg ctg ctg gtg Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val	1008
325 330 335	
aac gat gtc ctg gcc tct tgc tac gcg gtt ctg gag agt cac cag tgg Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp	1056
340 345 350	

gcg cac cgc gct ttt gcc ccc ttg aga ctg ctg cac gcg cta ggg gcg Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala	355	360	365	1104
ctg ctc ccc ggc ggg gcc gtc cag ccg act ggc atg cat tgg tac tct Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser	370	375	380	1152
cg ^g ctc ctc tac cgc tta gc ^g gag gag cta ctg ggc tg Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly	385	390	395	1190
<210> 9				
<211> 1251				
<212> DNA				
<213> Brachydanio rerio				
<220>				
<221> CDS				
<222> (1)...(1248)				
<400> 9				
atg gac gta agg ctg cat ctg aag caa ttt gct tta ctg tgt ttt atc Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile	1	5	10	15
agc ttg ctt ctg acg cct tgt gga tta gcc tgt ggt cct ggt aga ggt Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly	20	25	30	96
tat gga aaa cga aga cac cca aag aaa tta acc ccg ttg gct tac aag Tyr Gly Lys Arg Arg His Pro Lys Leu Thr Pro Leu Ala Tyr Lys	35	40	45	144
caa ttc atc ccc aac gtt gct gag aaa acg ctt gga gcc agc ggc aaa Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys	50	55	60	192
tac gaa ggc aaa atc aca agg aat tca gag aga ttt aaa gag ctg att Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile	65	70	75	80
ccg aat tat aat ccc gat atc atc ttt aag gac gag gaa aac aca aac Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn	85	90	95	288
gct gac agg ctg atg acc aag cgc tgt aag gac aag tta aat tcg ttg Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu	100	105	110	336
gcc ata tcc gtc atg aac cac tgg ccc ggc gtg aaa ctg cgc gtc act Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr	115	120	125	384
gaa ggc tgg gat gag gat ggt cac cat tta gaa gaa tct ttg cac tat Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr	130	135	140	432

gag gga cgg gca gtg gac atc act acc tca gac agg gat aaa agc aag Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys 145	150	155	160	480
tat ggg atg cta tcc agg ctt gca gtg gag gca gga ttc gac tgg gtc Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val 165	170	175		528
tat tat gaa tct aaa gcc cac ata cac tgc tct gtc aaa gca gaa aat Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn 180	185	190		576
tca gtg gct gct aaa tca gga gga tgt ttt cct ggg tct ggg acg gtg Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val 195	200	205		624
aca ctt ggt gat ggg acg agg aaa ccc atc aaa gat ctt aaa gtg ggc Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly 210	215	220		672
gac cgg gtt ttg gct gca gac gag aag gga aat gtc tta ata agc gac Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp 225	230	235	240	720
ttt att atg ttt ata gac cac gat ccg aca acg aga agg caa ttc atc Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile 245	250	255		768
gtc atc gag acg tca gaa cct ttc acc aag ctc acc ctc act gcc gcg Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala 260	265	270		816
cac cta gtt ttc gtt gga aac tct tca gca gct tcg ggt ata aca gca His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala 275	280	285		864
aca ttt gcc agc aac gtg aag cct gga gat aca gtt tta gtg tgg gaa Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu 290	295	300		912
gac aca tgc gag agc ctc aag agc gtt aca gtg aaa agg att tac act Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr 305	310	315	320	960
gag gag cac gag ggc tct ttt gcg cca gtc acc gcg cac gga acc ata Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile 325	330	335		1008
ata gtg gat cag gtg ttg gca tcg tgc tac gcg gtc att gag aac cac Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His 340	345	350		1056
aaa tgg gca cat tgg gct ttt gcg ccg gtc agg ttg tgt cac aag ctg Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu 355	360	365		1104

atg acg tgg ctt ttt ccg gct cgt gaa tca aac gtc aat ttt cag gag		1152	
Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu			
370	375	380	
gat ggt atc cac tgg tac tca aat atg ctg ttt cac atc ggc tct tgg		1200	
Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp			
385	390	395	400
ctg ctg gac aga gac tct ttc cat cca ctc ggg att tta cac tta agt		1248	
Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser			
405	410	415	
tga		1251	
<210> 10			
<211> 425			
<212> PRT			
<213> Gallus sp.			
<400> 10			
Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile			
1	5	10	15
Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly			
20	25	30	
Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys			
35	40	45	
Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg			
50	55	60	
Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr			
65	70	75	80
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly			
85	90	95	
Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu			
100	105	110	
Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr			
115	120	125	
Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr			
130	135	140	
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys			
145	150	155	160
Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val			
165	170	175	
Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn			
180	185	190	
Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val			
195	200	205	

His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
 210 215 220
 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
 225 230 235 240
 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
 245 250 255
 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
 260 265 270
 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
 275 280 285
 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
 290 295 300
 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
 305 310 315 - 320
 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
 325 330 335
 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
 340 345 350
 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
 355 360 365
 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
 370 375 380
 Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
 385 390 395 400
 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
 405 410 415
 Pro Leu Gly Met Val Ala Pro Ala Ser
 420 425
 <210> 11
 <211> 396
 <212> PRT
 <213> Murine sp.
 <400> 11
 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1 5 10 15
 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
 20 25 30
 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45

Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60

Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80

Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95

Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
 100 105 110

Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125

Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
 130 135 140

Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
 145 150 155 160

Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
 165 170 175

Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
 180 185 190

Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
 195 200 205

Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
 210 215 220

Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
 225 230 235 240

Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
 245 250 255

Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
 260 265 270

Val Phe Ala Ala Arg Gly Pro Ala Pro Gly Asp Phe Ala Pro
 275 280 285

Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
 290 295 300

Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
 305 310 315 320

Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
 325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
 340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
 355 360 365
 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
 370 375 380
 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
 385 390 395
 <210> 12
 <211> 411
 <212> PRT
 <213> Murine sp.
 <400> 12
 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
 1 5 10 15
 Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
 20 25 30
 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45
 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50 55 60
 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80
 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95
 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110
 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125
 Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
 130 135 140
 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
 145 150 155 160
 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
 165 170 175
 Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
 180 185 190
 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
 195 200 205
 Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys
 210 215 220

Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
 225 230 235 240

 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
 245 250 255

 Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
 260 265 270

 Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala
 275 280 285

 His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
 290 295 300

 Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
 305 310 315 320

 Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly
 325 330 335

 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
 340 345 350

 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
 355 360 365

 Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
 370 375 380

 Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr
 385 390 395 400

 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410

 <210> 13
 <211> 437
 <212> PRT
 <213> Murine sp.

 <400> 13
 Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
 1 5 10 15

 Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
 20 25 30

 Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
 35 40 45

 Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
 50 55 60

 Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
 65 70 75 80

Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp
 85 90 95

Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile
 100 105 110

Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125

Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly
 130 135 140

Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly
 145 150 155 160

Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
 165 170 175

Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val
 180 185 190

Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu
 195 200 205

Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg
 210 215 220

Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu
 225 230 235 240

Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile
 245 250 255

Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu
 260 265 270

Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser
 275 280 285

Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val
 290 295 300

Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser
 305 310 315 320

Val Thr Leu Arg Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala
 325 330 335

His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val
 340 345 350

Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu
 355 360 365

Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly
 370 375 380

Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly
 385 390 395 400

Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His
 405 410 415

Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met
 420 425 430

Ala Val Lys Ser Ser
 435

<210> 14
 <211> 418
 <212> PRT
 <213> Brachydanio rerio

<400> 14
 Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
 1 5 10 15

Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
 20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
 35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
 50 55 60

Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
 65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
 85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
 100 105 110

Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
 115 120 125

Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg
 130 135 140

Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr
 145 150 155 160

Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
 165 170 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
 180 185 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln
 195 200 205

Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val
 210 215 220

Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met
 225 230 235 240

Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu
 245 250 255

Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu
 260 265 270

Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala
 275 280 285

Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp
 290 295 300

Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu
 305 310 315 320

Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val
 325 330 335

Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu
 340 345 350

Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser
 355 360 365

Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn
 370 375 380

Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr
 385 390 395 400

Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn
 405 410 415

Ser Ser

<210> 15
 <211> 475
 <212> PRT
 <213> Homo sapien

<220>
 <221> MOD_RES
 <222> (463)
 <223> any or unknown amino acid

<400> 15
 Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu
 1 5 10 15

Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
 20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
 35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
 50 55 60

Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
 65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
 85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser
 100 105 110

Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
 115 120 125

Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg
 130 135 140

Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met
 145 150 155 160

Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
 165 170 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
 180 185 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu
 195 200 205

Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val
 210 215 220

Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr
 225 230 235 240

Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu
 245 250 255

Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu
 260 265 270

Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser
 275 280 285

Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu
 290 295 300

Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu
 305 310 315 320

Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr
 325 330 335

Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly
 340 345 350
 Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu
 355 360 365
 Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His
 370 375 380
 Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp
 385 390 395 400
 Ser Gly Gly Asp Arg Gly Gly Gly Arg Val Ala Leu Thr
 405 410 415
 Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
 420 425 430
 His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
 435 440 445
 Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
 450 455 460
 Arg Gly Ala Gly Gly Ala Arg Glu Gly Ala
 465 470 475
 <210> 16
 <211> 411
 <212> PRT
 <213> Homo sapien
 <400> 16
 Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu
 1 5 10 15
 Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg
 20 25 30
 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45
 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50 55 60
 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80
 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95
 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110
 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125

Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
 130 135 140
 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
 145 150 155 160
 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
 165 170 175
 Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
 180 185 190
 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
 195 200 205
 Gln Val Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg
 210 215 220
 Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe
 225 230 235 240
 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala
 245 250 255
 Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
 260 265 270
 Pro Ala His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala
 275 280 285
 Arg Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
 290 295 300
 Leu Val Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
 305 310 315 320
 Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly
 325 330 335
 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
 340 345 350
 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His
 355 360 365
 Ser Leu Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr
 370 375 380
 Pro Gln Leu Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Gly Ser
 385 390 395 400
 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410

<210> 17
 <211> 396
 <212> PRT
 <213> Homo sapien

<400> 17

Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1 5 10 15

Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
 20 25 30

Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45

Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60

Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80

Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95

Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
 100 105 110

Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125

Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
 130 135 140

Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
 145 150 155 160

Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
 165 170 175

Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu
 180 185 190

Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
 195 200 205

Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
 210 215 220

Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu
 225 230 235 240

Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
 245 250 255

Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
 260 265 270

Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
 275 280 285

Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
 290 295 300

Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
 305 310 315 320

Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
 325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
 340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
 355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
 370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
 385 390 395

<210> 18
 <211> 416
 <212> PRT
 <213> Brachydanio rerio

<400> 18
 Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
 1 5 10 15

Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
 20 25 30

Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
 35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
 50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
 65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
 85 90 95

Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
 100 105 110

Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
 115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr
 130 135 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys
 145 150 155 160

Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
 165 170 175

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
 180 185 190

Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val
 195 200 205

Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly
 210 215 220

Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp
 225 230 235 240

Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile
 245 250 255

Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala
 260 265 270

His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala
 275 280 285

Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu
 290 295 300

Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr
 305 310 315 320

Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile
 325 330 335

Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His
 340 345 350

Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu
 355 360 365

Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu
 370 375 380

Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp
 385 390 395 400

Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser
 405 410 415

<210> 19

<211> 1416

<212> DNA

<213> Drosophila sp.

<220>

<221> CDS

<222> (1)...(1413)

<400> 19

atg gat aac cac agc tca gtg cct tgg gcc agt gcc gcc agt gtc acc
 Met Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr

1

5

10

15

48

tgt ctc tcc ctg gga tgc caa atg cca cag ttc cag ttc cag Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln	96
20 25 30	
ctc caa atc cgc agc gag ctc cat ctc cgc aag ccc gca aga aga acg Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr	144
35 40 45	
caa acg atg cgc cac att gcg cat acg cag cgt tgc ctc agc agg ctg Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu	192
50 55 60	
acc tct ctg gtg gcc ctg ctg atc gtc ttg ccg atg gtc ttt agc Thr Ser Leu Val Ala Leu Leu Ile Val Leu Pro Met Val Phe Ser	240
65 70 75 80	
ccg gct cac agc tgc ggt cct ggc cga gga ttg ggt cgt cat agg gcg Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala	288
85 90 95	
cgc aac ctg tat ccg ctg gtc ctc aag cag aca att ccc aat cta tcc Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser	336
100 105 110	
gag tac acg aac agc gcc tcc gga cct ctg gag ggt gtg atc cgt cgg Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg	384
115 120 125	
gat tcg ccc aaa ttc aag gac ctc gtg ccc aac tac aac agg gac atc Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile	432
130 135 140	
ctt ttc cgt gac gag gaa ggc acc gga gcg gat ggc ttg atg agc aag Leu Phe Arg Asp Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys	480
145 150 155 160	
ccg tgc aag gag aag cta aac gtg ctg gcc tac tcg gtg atg aac gaa Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu	528
165 170 175	
tgg ccc ggc atc cgg ctg ctg gtc acc gag agc tgg gac gag gac tac Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr	576
180 185 190	
cat cac ggc cag gag tcg ctc cac tac gag ggc cga gcg gtg acc att His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile	624
195 200 205	
gcc acc tcc gat cgc gac cag tcc aaa tac ggc atg ctc gct cgc ctg Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu	672
210 215 220	
gcc gtc gag gct gga ttc gat tgg gtc tcc tac gtc agc agg cgc cac Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His	720
225 230 235 240	

atc tac tgc tcc gtc aag tca gat tcg tcg atc agt tcc cac gtg cac Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His 245	250	255	768	
ggc tgc ttc acg ccg gag agc aca gcg ctg ctg gag agt gga gtc cgg Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg 260	265	270	816	
aag ccg ctc ggc gag ctc tct atc gga gat cgt ttg agc atg acc Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr 275	280	285	864	
gcc aac gga cag gcc gtc tac agc gaa gtg atc ctc ttc atg gac cgc Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg 290	295	300	912	
aac ctc gag cag atg caa aac ttt gtg cag ctg cac acg gac ggt gga Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly 305	310	315	320	960
gca gtg ctc acg gtg acg ccg gct cac ctg gtt agc gtt tgg cag ccg Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro 325	330	335	1008	
gag agc cag aag ctc acg ttt gtg ttt gcg cat cgc atc gag gag aag Glu Ser Gln Lys Leu Thr Phe Val Ala His Arg Ile Glu Glu Lys 340	345	350	1056	
aac cag gtg ctc gta cgg gat gtg gag acg ggc gag ctg agg ccc cag Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln 355	360	365	1104	
cga gtg gtc aag ttg ggc agt gtg cgc agt aag ggc gtg gtc gcg ccg Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro 370	375	380	1152	
ctg acc cgc gag ggc acc att gtg gtc aac tcg gtg gcc gcc agt tgc Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys 385	390	395	400	1200
tat gcg gtg atc aac agt cag tcg ctg gcc cac tgg gga ctg gct ccc Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro 405	410	415	1248	
atg cgc ctg ctg tcc acg ctg gag gcg tgg ctg ccc gcc aag gag cag Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln 420	425	430	1296	
ttg cac agt tcg ccg aag gtg gtg agc tcg gcg cag cag cag aat ggc Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly 435	440	445	1344	
atc cat tgg tat gcc aat gcg ctc tac aag gtc aag gac tac gtg ctg Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu 450	455	460	1392	

1416

ccg cag agc tgg cgc cac gat tga
 Pro Gln Ser Trp Arg His Asp
 465 470

<210> 20
 <211> 471
 <212> PRT
 <213> Drosophila sp.

<400> 20
 Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
 1 5 10 15

Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln
 20 25 30

Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr
 35 40 45

Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu
 50 55 60

Thr Ser Leu Val Ala Leu Leu Ile Val Leu Pro Met Val Phe Ser
 65 70 75 80

Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala
 85 90 95

Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser
 100 105 110

Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg
 115 120 125

Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile
 130 135 140

Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys
 145 150 155 160

Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu
 165 170 175

Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr
 180 185 190

His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile
 195 200 205

Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu
 210 215 220

Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His
 225 230 235 240

Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His
 245 250 255

Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg
 260 265 270

Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr
 275 280 285

Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg
 290 295 300

Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly
 305 310 315 320

Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro
 325 330 335

Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys
 340 345 350

Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln
 355 360 365 -

Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro
 370 375 380

Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys
 385 390 395 400

Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro
 405 410 415

Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
 420 425 430

Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
 435 440 445

Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
 450 455 460

Pro Gln Ser Trp Arg His Asp
 465 470

<210> 21
<211> 221
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
polypeptide sequence

<220>
<221> MOD_RES
<222> 7
<223> Gly, Ala, Val, Leu, Ile, Phe, Tyr or Trp

```
<220>
<221> MOD_RES
<222> 9
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 44
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 85
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 93
<223> Lys, Arg, His, Asn or Gln

<220>
<221> MOD_RES
<222> 98
<223> Lys, Arg or His

<220>
<221> MOD_RES
<222> 112
<223> Ser, Thr, Tyr, Trp or Phe

<220>
<221> MOD_RES
<222> 132
<223> Lys, Arg or His

<220>
<221> MOD_RES
<222> 137
<223> Met, Cys, Ser or Thr

<220>
<221> MOD_RES
<222> 139
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 181
<223> Leu, Val, Met, Thr or Ser

<220>
<221> MOD_RES
<222> 183
<223> His, Phe, Tyr, Ser, Thr, Met or Cys

<220>
<221> MOD_RES
<222> 185
```

<223> Gln, Asn, Glu, or Asp

<220>

<221> MOD_RES

<222> 186

<223> His, Phe, Tyr, Thr, Gln, Asn, Glu or Asp

<220>

<221> MOD_RES

<222> 189

<223> Gln, Asn, Glu, Asp, Thr, Ser, Met or Cys

<220>

<221> MOD_RES

<222> 191

<223> Ala, Gly, Cys, Leu, Val or Met

<220>

<221> MOD_RES

<222> 196

<223> Arg, Lys, Met, Ile, Asn, Asp, Glu, Gln, Ser, Thr or Cys

<220>

<221> MOD_RES

<222> 200

<223> Arg, Lys, Met or Ile

<220>

<221> MOD_RES

<222> 206

<223> Ala, Gly, Cys, Asp, Glu, Gln, Asn, Ser, Thr or Met

<220>

<221> MOD_RES

<222> 207

<223> Ala, Gly, Cys, Asp, Asn, Glu or Gln

<220>

<221> MOD_RES

<222> 209

<223> Arg, Lys, Met, Ile, Asn, Asp, Glu or Gln

<220>

<221> MOD_RES

<222> 211

<223> Leu, Val, Met or Ile

<220>

<221> MOD_RES

<222> 212

<223> Phe, Tyr, Thr, His or Trp

<220>

<221> MOD_RES

<222> 216

<223> Ile, Val, Leu or Met

<220>

<221> MOD_RES
 <222> 217
 <223> Met, Cys, Ile, Leu, Val, Thr or Ser

<220>
 <221> MOD_RES
 <222> 219
 <223> Leu, Val, Met, Thr or Ser

<220>
 <223> each Xaa may also be any amino acid.

<400> 21
 Cys Gly Pro Gly Arg Gly Xaa Gly Xaa Arg Arg His Pro Lys Lys Leu
 1 5 10 15

Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr
20															30

Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Xaa	Arg	Asn	Ser	Glu
35															45

Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys
50															60

Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys
65															80

Asp	Lys	Leu	Asn	Xaa	Leu	Ala	Ile	Ser	Val	Met	Asn	Xaa	Trp	Pro	Gly
85															95

Val	Xaa	Leu	Arg	Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Xaa
100															110

Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser
115															125

Asp	Arg	Asp	Xaa	Ser	Lys	Tyr	Gly	Xaa	Leu	Xaa	Arg	Leu	Ala	Val	Glu
130															140

Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys
145															160

Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe
165															175

Pro	Gly	Ser	Ala	Xaa	Val	Xaa	Leu	Xaa	Xaa	Gly	Gly	Xaa	Lys	Xaa	Val
180															190

Lys	Asp	Leu	Xaa	Pro	Gly	Asp	Xaa	Val	Leu	Ala	Ala	Asp	Xaa	Xaa	Gly
195															205

Xaa	Leu	Xaa	Xaa	Ser	Asp	Phe	Xaa	Xaa	Phe	Xaa	Asp	Arg			
210															220

<210> 22
 <211> 167

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate polypeptide sequence

<220>
<221> MOD_RES
<222> 7
<223> Gly, Ala, Val, Leu, Ile, Pro, Phe or Tyr

<220>
<221> MOD_RES
<222> 8
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> 9
<223> Gly, Ala, Val, Leu, Ile, Lys, His or Arg

<220>
<221> MOD_RES
<222> 12
<223> Lys, Arg or His

<220>
<221> MOD_RES
<222> 13
<223> Phe, Trp, Tyr or an amino acid gap

<220>
<221> MOD_RES
<222> 14
<223> Gly, Ala, Val, Leu, Ile or an amino acid gap

<220>
<221> MOD_RES
<222> 17
<223> Asn, Gln, His, Arg or Lys

<220>
<221> MOD_RES
<222> 19
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 22
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 27
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<221> MOD_RES
<222> 29
<223> Ser, Thr, Gln or Asn

<220>
<221> MOD_RES
<222> 30
<223> Met, Cys, Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 31
<223> Gly, Ala, Val, Leu, Ile or Pro

<220>
<221> MOD_RES
<222> 33
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 40
<223> Gly, Ala, Val, Leu, Ile, Pro, Arg, His or Lys

<220>
<221> MOD_RES
<222> 41
<223> Gly, Ala, Val, Leu, Ile, Phe or Tyr

<220>
<221> MOD_RES
<222> 44
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 45
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 46
<223> Thr or Ser

<220>
<221> MOD_RES
<222> 48
<223> Gly, Ala, Val, Leu, Ile, Asn or Gln

<220>
<221> MOD_RES
<222> 53
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 54
<223> Asp or Glu

<220>
<221> MOD_RES
<222> 71
<223> Ser or Thr

<220>
<221> MOD_RES
<222> 79
<223> Glu, Asp, Gln or Asn

<220>
<221> MOD_RES
<222> 83
<223> Glu or Asp

<220>
<221> MOD_RES
<222> 84
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 85
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> 87
<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
<221> MOD_RES
<222> 95
<223> Met, Cys, Gln, Asn, Arg, Lys or His

<220>
<221> MOD_RES
<222> 100
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 107
<223> Trp, Phe, Tyr, Arg, His or Lys

<220>
<221> MOD_RES
<222> 114
<223> Gly, Ala, Val, Leu, Ile, Ser, Thr, Tyr or Phe

<220>
<221> MOD_RES
<222> 115
<223> Gln, Asn, Asp or Glu

<220>
<221> MOD_RES

<222> 116
<223> Asp or Glu

<220>
<221> MOD_RES
<222> 125
<223> Gly, Ala, Val, Leu, or Ile

<220>
<221> MOD_RES
<222> 134
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 135
<223> Asn, Gln, Thr or Ser

<220>
<221> MOD_RES
<222> 139
<223> Gly, Ala, Val, Leu, Ile, Ser, Thr, Met or Cys

<220>
<221> MOD_RES
<222> 141
<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
<221> MOD_RES
<222> 157
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 158
<223> Asn, Gln, Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> 160
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> 162
<223> Gly, Ala, Val, Leu, Ile, Ser, Thr or Cys

<220>
<221> MOD_RES
<222> 166
<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
<221> MOD_RES
<222> 167
<223> Asp or Glu

<400> 22
 Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys
 1 5 10 15

Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu
 20 25 30

Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa
 35 40 45

Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile
 50 55 60

Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg
 65 70 75 80

Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp
 85 90 95

Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His
 100 105 110 -

His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr
 115 120 125

Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala
 130 135 140

Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa
 145 150 155 160

His Xaa Ser Val Lys Xaa Xaa
 165

<210> 23
 <211> 74
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 23
 gcgcgcttcg aagcgaggca gccagcgagg gagagagcga gcgggcgagc cggagcgagg 60
 aaatcgatgc gcmc 74

<210> 24
 <211> 74
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 24

gcgcgcaagat ctgggaaagc gcaagagaga ggcgcacacgc acacacccgc cgcgcgact 60
 cgggatccgc gcgc 74

<210> 25
 <211> 996
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: gene activation construct

<400> 25
 cgaagcgagg cagccagcga gggagagagc gagcgggcga gccggagcga ggaaatcgaa 60
 ggttcgaatc cttccccac caccatcaact ttcaaaaagtc cgaaaagaatc tgctccctgc 120
 ttgtgtttg gaggtcgctg agtagtgcgc gagtaaaatt taagctacaa caaggcaagg 180
 cttgaccgac aattgcatga agaatctgct tagggtagg cgtttgcgc tgcttcgcga 240
 tgcggggcc agatatacgc gttgacattt attattgact agttattaaat agtaatcaat 300
 tacggggtca ttagttcata gcccataatat ggagttccgc gttacataac ttacggtaaa 360
 tggcccgccct ggctgaccgc ccaacgaccc cccgcattt acgtcaataa tgacgtatgt 420
 tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggact atttacggta 480
 aactgcccac ttggcagtac atcaagtgtt tcatatgccaa agtacgcccc ctattgacgt 540
 caatgacggt aaatggcccg cctggcatta tgcccagtac atgaccttat gggactttcc 600
 tacttggcag tacatctacg tattagtcat cgctattacc atggtgatgc gggtttggca 660
 gtacatcaat gggcgtggat agcggtttga etcacggggta tttccaagtc tccacccat 720
 tgacgtcaat gggagtttgt tttggcacca aaatcaacgg gactttccaa aatgtcgtaa 780
 caactccgccc ccattgacgc aaatggccgg taggcgtgtt cgggtggagg tctatataag 840
 cagagctctc tggctaacta gagaacccac tgcttactgg cttatcgaaa ttaatacgcac 900
 tcactatagg gagacccaag cttggtaccg agctcgatc gatctggaa agcgcaagag 960
 agagcgacaca cgacacacacc cgccgcgc actcg 996

<210> 26
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: antisense construct

<400> 26
gtcctggcgcc cgccgcccgtcgcc

26

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: antisense construct

<400> 27
ttccgatgac cggccttcg cggtga

26

<210> 28
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: antisense construct

<400> 28
gtgcacggaa aggtgcaggc cacact

26

<210> 29
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 29
ggctccggta tgtgc

15

<210> 30
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 30
ggggtacttc agggt

15

<210> 31
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 31

cattggcagg aggagttgat tgtgg

25

<210> 32

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 32

agcaccccttt gagtggagtt tgggg

25